

**Plot of Icl|31669 vs gi|42541062|gb|AAS19428.1| [?]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Sequences producing significant alignments:	Score (Bits)	E Value
gb AAS19428.1  anti-SARS S protein immunoglobulin light chain...	144	4e-40

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>gb|AAS19428.1| anti-SARS S protein immunoglobulin light chain variable region  
[Homo sapiens]  
Length=106

Score = 144 bits (362), Expect = 4e-40, Method: Compositional matrix adjust.  
Identities = 70/104 (67%), Positives = 85/104 (81%), Gaps = 0/104 (0%)

Query 4	MTQSPSSLSASLGDRTVITSCRASQDISNYLNWYQQKPDGTVKLLIYTSRLHAGVPSRFS	63
Sbjct 3	MTQSPSSLSAS+GDRVTI+CRA+Q IS +LNWYQQ+ KLLIY S L +GVPSRFS	62
Query 64	GSGSGTDXSLTISNLQEQEDIATYFCQQGYTLPYIFGGGTKLEIK	107
Sbjct 63	GSGSGT+++LTIS+L+ ED ATY+C Q + P+TGF GT +EIK	106
	GSGSGTEFTLTISSLQPEDFATYYCLQHRSYPWTFQGQTNVEIK	

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